

Qy 41 ArgLeuProHleGlyHis***HisLeuLeuysAspLysLeuLeuHisTyrAla*** 60
 Db 174 CGCTCTCCCTTCATGACACCTTCACTTAAAGACAACTTCTCCATCGACATC 233
 Qy 61 IleAspLeuSerLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
 Db 234 ATGACCTCTCAAAAACATGATGCTTATCTCTCTACTTGGCTCCATGACACCC 293
 Qy 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
 Db 294 GTTGTGCTCCACACACAGATTTTCAAGCTTCTCTCCAAACGACAGAGGACCTTC 353
 Qy 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
 Db 354 TTCAACCAAGATCCAAACCTCAAGCCATTAAGACGCTCATGATAGTCAAGTGGCC 413
 Qy 121 *****Pro***GlyProTyrTrp***PheValArgLysLeuLeuMetAsnAspLeu 140
 Db 414 ATGCTTCCCTTCGACCTTACTGGAAGTTCGTGAGAGAGCTCATGACACCTTCCC 473
 Qy 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnIleArgLys***Leu 160
 Db 474 AAGCGACACACTGTAACAGTTGAGGCTTTGAGAGACCAACGACACCCGACAGTCTT 533
 Qy 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluLeuLeu 180
 Db 534 AGGTATGGCCCAAGAGCGGACAGACGACGACCCCTTACCTACACAGAGCTTCTG 593
 Qy 181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluLysIleArgAsp 200
 Db 594 AAATGACCAACAGCACATCTCATGATGATGCTCGGCGAGGCTGAGAGATCAGAGAC 653
 Qy 201 IleAlaArgLysValLeuLysIle***GlyLysTyrSerLeuThrAspPheIle***Pro 220
 Db 654 ATCGCTGCGAGGTCTTAAAGATCTTGGCAATACAGCTCATGACTTCACTCTGCCA 713
 Qy 221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
 Db 714 TTGAGCATCTCAAGGTTGAAAGTATGAGAGAGATCGACACATTTGAAACAAGTTC 773
 Qy 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
 Db 774 GACCTGTCTGTAAGAGGTCTATCAAGAGCGGCTGAGATCTGAGAGAGAAAGAAC 833
 Qy 261 GlyLys*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
 Db 834 GGAGAGGTTGTGAGGAGGTCAAGCGGGGTTTCTTGACACTTGTGAAATCCGT 893
 Qy 281 GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp 300
 Db 894 GAGGATAGACATGAGATCAAAATCAACAGACCAACGACGAGGCTTGTGTGAC 953
 Qy 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuLysIleGlu 320
 Db 954 TTTTCTCGGACGAAACGACTCCACAGCGGTGCGAACAGATGGGCAATTGGCAACTC 1013

Qy 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
 Db 1014 ATCAACAATCTTGAAGGTGTGAAAAGGCTCTGAGAGAGGTCTACAGTGTGGGAAAG 1073
 Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
 Db 1074 GACACATCTTGACAGAAAGTTGACACTCAAAACCTTCTTACATTAGACAACTCGAAG 1133
 Qy 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGlyCys 380
 Db 1134 GAGCATTCGCGATGAGACCCGACCTCCAGATGTGCAAAAGAAATGACAGAAAGTGT 1193
 Qy 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
 Db 1194 GAGATTATGATATGTGATCTCCAGAGAGGATGATTTCTCTCATATGATGACAGTA 1253
 Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
 Db 1254 GGAAGAGACCCCAAAATCTGGAGACAGACCATGAGTTCGTCGTGAGAGGTTCTAG 1313
 Qy 421 Thr***AlaGluGlyValAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
 Db 1314 ACGAGGCTGTGAAGGAGAGACAGGCGCTTATCTTGAAGGAGACAACTTTCAACTTCTC 1373
 Qy 441 PropheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
 Db 1374 CCATTGGGCTCGAGAGAGATGTGCTCGAGATCAATGGCTACTTGGAGATGGCA 1433
 Qy 461 ThrLeuLeuAlaSerLeuLeuGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
 Db 1434 ACACTTCTTCATCTCTTATTAAGTGTCTGACTTGCATGCAATGCTGGGTCACAAAGAC 1493
 Qy 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
 Db 1494 ATATTGAAGGTGTGAGCGCAAGATTACATGAGAGAGAGCGGCTCACTGTTCCA 1553
 Qy 501 ArgAlaHisSerLeuValCysValProLeuAlaArgGlyValAlaSerLysLeuLeu 520
 Db 1554 AAGGACACTAGTCTTGTGTGTGTTCCACTTGCAGAGATCGGCGTTGCATTAACCTCTT 1613
 Qy 521 Ser 521
 Db 1614 TCT 1616

RESULT 11
 AAA72444
 ID AAA72444 standard; cDNA, 1824 BP.
 XX
 AC AAA72444;
 XX
 DT 19-DEC-2000 (first entry)
 XX
 DE Soybean CYP3A1 isoflavone synthase cDNA.
 KW Soybean; CYP3A1; cytochrome P450; isoflavone synthase;
 KW isoflavonoid biosynthesis; phenylpropanoid pathway; leguminous plant;
 KW defence response; attractant; repellent; signal compound; antibiotic;

Key Location/Qualifiers
 CDS 36..1601
 FT /tag=a
 FT /product= "isoflavone synthase reaction enzyme"
 XX MO20053771-A1.
 XX 14-SEP-2000.
 XX 08-MAR-2000; 2000MO-US05915.
 XX 08-MAR-1999; 99US-0123267.
 XX (ROBE-) ROBERTS NOBLE FOUND INC SAMMUEL.
 XX Steele CL, Dixon RA;
 XX WPI: 2000-594325/56.
 XX P-PSDB: AAB18613.
 XX Genetic manipulation of naturally non-isoflavonoid producing plants by
 PT introducing a DNA segment encoding an enzyme catalyzing the aryl
 PT migration of flavanone to form an isoflavanone intermediate
 XX
 XX Claim 74; Fig 2; 74pp; English.
 XX
 CC The present sequence encodes a soybean enzyme, which catalyzes the
 CC first step of the isoflavone synthase reaction. The enzyme is a
 CC cytochrome P450 that can catalyze the aryl migration of a flavanone to
 CC isoflavone. The gene is designated CYP93C. The specification describes
 CC a method for genetically engineering naturally non-isoflavonoid producing
 CC plant species to produce isoflavone intermediates or isoflavones. The
 CC method involves introducing CYP93C DNA sequences into plants. The
 CC transgenic plants are useful for producing isoflavonoids, which are
 CC useful as food. The gene is used for increasing disease resistance in
 CC a plant, increasing nodulation efficiency of a leguminous plant and
 CC increasing bacterial or fungal symbiosis in a plant. Engineering
 CC constitutive production of daidzein and/or genistein or their
 CC conjugates into tomato, potato, corn or other popular components of
 CC the human diet leads to reduced cancer risk, reduced incidence of
 CC osteoporosis and treatment for alcoholism. Modifying the extent of
 CC production of isoflavonoids in legume roots positively impacts nodulation
 CC efficiency and as a result plant yield.
 XX
 SQ Sequence 1717 BP; 465 A; 422 C; 407 G; 423 T; 0 other;

Alignment Scores:
 Pred. No.: 3.73e-272 Length: 1717
 Score: 2267.00 Matches: 454
 Percent Similarity: 87.14% Conservative: 0
 Best Local Similarity: 87.14% Mismatches: 67
 Query Match: 94.62% Indels: 0
 Db: 21 Gaps: 0
 US-09-857-581-66 (1-521) x AAA75430 (1-1717)
 QY 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuAlaGPro 20

Db 36 ATGTGCTTAACCTGCACTGCTTATGCTTGGCTGCTTCTGCTGCACTTCGCTCC 95
 QY 21 ThrPro***Ala***SerIysAlaLeuArgHisLeuProAsnProPheSerPro***Pro 40
 Db 96 ACACCACTGCAAAATCAAAAGCACTTGGCATCTCCCAAAACCAACCAAGCCAAAGCT 155
 QY 41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
 Db 156 CGCTTCCTCCCTCAATAGACACTTCATCTTTAAAGACAAACCTTCACATCGCACTC 215
 QY 61 IleAspLeuSerLysLysHisGlyProLeuPheSer****PheGlySerMetProThr 80
 Db 216 ATGACCTCTCCAAAACATAGTCCCTTATTTCTCTCACTTGGCTCCATCCCAACC 275
 QY 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln****GluAlaThrSer 100
 Db 276 GTTGTGCTCTCCACACCAAAATGTTCAAGCTTCTTCCAAAGCAGACCAACTTCC 335
 QY 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp****ValAla 120
 Db 336 TTCAACACAGAGTTCCAAACTCCAGCATAGAGGCTCACTATGATGCTCAGTGGCC 395
 QY 121 *****Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeu 140
 Db 396 ATGCTTCCTCCGACCTTACGACCTTACGACCTTACGACCTTACGACCTTACGACCTT 455
 QY 141 AsnAlaThrThrValAsp***LeuArgProLeuArgThrGlnIleAlaLys***Leu 160
 Db 456 AAGCGACCACTGTAACAAAGTAGAGCTTTAGAGACCCCAACAGATCCGAGACTTCTT 515
 QY 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluLysLeu 180
 Db 516 AGGTTATGCGCCCAAGCGACAGAGGACAGAGCCCTTCACTTACCGAGACTTCTG 575
 QY 181 LysTrp***AsnSerThr***SerMetMet***LeuGlyLysAlaGluLysIleArgAsp 200
 Db 576 AATGACCAACAGACCACTTCATGATGATGCTGCGAGGCTGAGGACATAGAGAC 635
 QY 201 IleAlaArgGluValLeuLysIle***GlyGlyLysSerLeuThrAspPheIle***Pro 220
 Db 636 ATGCTTCGCGAGGTTCTTAAAGATCTTTGGGGAATCAACCTTCATGACTTCACTGCGCA 695
 QY 221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
 Db 696 TTGAAGCATCTCAAGGTTGAAAGATGAGAGAGATCAAGCATCTTCAACAGACTTC 755
 QY 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
 Db 756 GACCTGCTGCTGAAGGCTCATCAAGAGCCCTGATGATGATGAGAGAGAGAGAGAG 815
 QY 261 GlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 280
 Db 816 GAGAGAGTTGATGAGGTCAGGCGGGGTTTCTTGACACTTCTGCTTGAATTCGCT 875
 QY 281 GluAspGluThr***GluIleLysIleThrLys****IleLysGlyLeuValValAsp 300